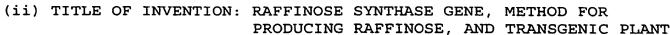
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: OSUMI Chieko NOZAKI Jinshi

KIDA Takao



- (iii) NUMBER OF SEQUENCES: 22
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 - (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 - (C) CITY: ARLINGTON
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: USA
 - (F) ZIP: 22202
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 - (vi) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: NORMAN F. OBLON
 - (B) REGISTRATION NUMBER: 24,618
- (vii) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703)-413-3000
 - (B) TELEFAX: (703)-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:1:

Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr Leu Thr Val His Pro Gln
1 5 10 15

Gly Val Ile Glu Gly Val Arg His Leu Val Asp Gly Gly Cys
20 25 30

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
 - (v) FRAGMENT TYPE: internal



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	Arg H INFORM (i) (i) (x) Asp INFORM (ii) (ii) (vi) (ix) (xi) AAACA CCT Pro AAT ASD CCT Pro CTTT SPhe GATT	Arg His INFORMAT: (ii) M (v) F (xi) S Asp Gln INFORMAT (i) SEQ (A (B (C) (II) MOL (VI) ORI (IX) FEA (IX) FEA (IX) SEQ AAACAAC CAAACAAC CAAACAAC CAAACAAC CAAACAAC	Arg His INFORMATION I (i) SEQUENCY (A) (B) (D) (ii) MOLECY (V) FRAGMY (Xi) SEQUENCY (Xi) SEQUENCY (A) LE (B) TY (C) ST (D) TO (ii) MOLECUL (Vi) ORIGINA (A) OR (ix) FEATURE (A) NA (B) LC (Xi) SEQUENCY (A) NA (B) LC (XI) SE	Val Ser Val Gly (Arg His INFORMATION FOR ((i) SEQUENCE ((A) LENG ((B) TYPE ((D) TOPE ((ii) MOLECULE ((v) FRAGMENT ((xi) SEQUENCE (Asp Gln Asp Gln ((i) SEQUENCE ((A) LENGTH ((B) TYPE: ((C) STRAND ((D) TOPOLO ((ii) MOLECULE TY ((vi) ORIGINAL SO ((A) ORGANI ((ix) FEATURE: ((A) NAME/K ((B) LOCATI ((xi) SEQUENCE DE (AAACAAC CCTTCTTTT ((Xi) SEQUENCE DE (AAACAAC CCTTCTTTT ((A) ASP Met Ser ((A) ASP	Val Ser Val Gly Cys F Arg His INFORMATION FOR SEQ I (i) SEQUENCE CHARM (A) LENGTH: (B) TYPE: an (D) TOPOLOGY (ii) MOLECULE TYPE (v) FRAGMENT TYPE (xi) SEQUENCE DESCI Asp Gln Asp Gln Met I (i) SEQUENCE CHARACY (i) SEQUENCE CHARACY (i) SEQUENCE CHARACY (i) SEQUENCE CHARACY (i) STRANDEDNE (D) TOPOLOGY: (ii) MOLECULE TYPE: (vi) ORIGINAL SOURCE (A) ORGANISM: (ix) FEATURE: (A) NAME/KEY: (B) LOCATION: (xi) SEQUENCE DESCRI AAACAAC CCTTCTTTTA GT (CCT AGT TTT AAA AAT PRO SER PHE LYS ASN AAAT GAC ATG TCG TCA ASN ASP MET SER SER 20 G AAC GGT CAT TCG TTT ASN Gly His SER PHE 35 CCT TCT CCG TAC ACT PRO SER PRO TYR THR 35 CTTT GTT GGA TTC GAC S PHE Val Gly PHE ASP 70 G ATT GGG AAG CTG AAG	Val Ser Val Gly Cys Phe V 5 Arg His INFORMATION FOR SEQ ID NO (i) SEQUENCE CHARACTEI (A) LENGTH: 14; (B) TYPE: amino (D) TOPOLOGY: 1: (ii) MOLECULE TYPE: pej (v) FRAGMENT TYPE: in (xi) SEQUENCE DESCRIPT Asp Gln Asp Gln Met Val 5 INFORMATION FOR SEQ ID No (i) SEQUENCE CHARACTERI (A) LENGTH: 2517 b (B) TYPE: nucleic (C) STRANDEDNESS: (D) TOPOLOGY: line (ii) MOLECULE TYPE: cDNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucu (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 56 (xi) SEQUENCE DESCRIPTION AAACAAC CCTTCTTTTA GTTTTT CCCT AGT TTT AAA AAT GGT PRO Ser Phe Lys Asn Gly 5 AAT GAC ATG TCG TCA CCG ASN ASP Met Ser Ser Pro 20 AAC GGT CAT TCG TTT CTG ASN Gly His Ser Phe Leu 35 40 CCT TCT CCG TAC ACT TCG PRO Ser Pro Tyr Thr Ser CTTT GTT GGA TTC GAC GCG S Phe Val Gly Phe Asp Ala 70 ATT GGG AAG CTG AAG GAT	Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERIST: (A) LENGTH: 14 amino (B) TYPE: amino acid (D) TOPOLOGY: linea: (ii) MOLECULE TYPE: peptido (v) FRAGMENT TYPE: interno: (xi) SEQUENCE DESCRIPTION: Asp Gln Asp Gln Met Val Val 5 INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTIC (A) LENGTH: 2517 base (B) TYPE: nucleic acid (C) STRANDEDNESS: doub (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SAACAAC CCTTCTTTTA GTTTTTTGGG CCT AGT TTT AAA AAT GGT GGC Pro Ser Phe Lys Asn Gly Gly 5 AAT GAC ATG TCG TCA CCG TTT ASN ASP Met Ser Ser Pro Phe 20 25 AAC GGT CAT TCG TTT CTG TCC ASN Gly His Ser Phe Leu Ser 35 40 CCT TCT CCG TAC ACT TCG ATA Pro Ser Pro Tyr Thr Ser Ile 5 C TTT GTT GGA TTC GAC GCG TCG 5 Phe Val Gly Phe Asp Ala Ser 70 G ATT GGG AAG CTG AAG GAT ATT	Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino accid (B) TYPE: amino accid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ Asp Gln Asp Gln Met Val Val Val (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2517 base pair (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (Cu (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SEQ I AAACAAC CCTTCTTTTA GTTTTTTGGG TTT CCCT AGT TTT AAA AAT GGT GGC TCC PRO SER PHE LYS ASN Gly Gly SER AAAT GAC ATG TCG TCA CCG TTT GCA ASN ASP Met SER SER PRO PHE Ala 20 25 AAAT GAC ATG TCG TCA CCG TTT GCA ASN Gly His SER PHE LEU SER ASP 35 CCT TCT CCG TAC ACT TCG ATA GAC CR PRO SER PRO TYR THR SER ILE ASP 35 CCTT TCT CCG TAC ACT TCG ATA GAC CR PRO SER PRO TYR THR SER ILE ASP 35 CCTT TCT CCG TAC ACT TCG ATA GAC CR PRO SER PRO TYR THR SER ILE ASP 35 CCTT TCT CCG TAC ACT TCG ATA GAC CR PRO SER PRO TYR THR SER ILE ASP 36 37 38 37 30 31 31 31 31 32 34 35 40 35 36 37 37 38 37 38 37 38 38 38 39 30 30 31 31 32 33 34 35 35 36 37 37 38 38 38 38 38 38 38 38	Val Ser Val Gly Cys Phe Val Gly Phe A 5 10 Arg His INFORMATION FOR SEQ ID NO:3:	Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3 Asp Gln Asp Gln Met Val Val Val Gln Val 1 5 10 INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2517 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA to mRNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (Cucumis sa (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTTCTT CCCT AGT TTT AAA AAT GGT GGC TCC AAC GTA (Pro Ser Phe Lys Asn Gly Gly Ser Asn Val (A) AAT GAC ATG TCG TCA CCG TTT GCA ATC GAC (A Asn Asp Met Ser Ser Pro Phe Ala Ile Asp (A) AAT GAC ATG TCG TTT CTG TCC GAT GTT CCT (A) ASN Gly His Ser Phe Leu Ser Asp Val Pro (B) CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC (C) TCT CCG TAC ACT TCG ATA GAC AAG TCC (C) TTT GTT GGA TTC GAC GTG TCG GAA CCT GAT (C) TCT CCG TAC ACT TCG ATA GAC AAG TCC (C) TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT (C) TCT CCG TAC ACT TCG ATA GAC AAG TCC (C) TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT (C) TCT CCG TAC ACT TCG ATA GAC AAG TCC (C) TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT (C) TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT (C) TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT (C) TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT (C) TTT GTT GGA AGC CTG AAG GAT ATT CGG TTT ATG	Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala S 5 10 Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: Asp Gln Asp Gln Met Val Val Gln Val Pro 7: 5 10 INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2517 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (Cucumis sativa (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTTCTT CTTT CCCT AGT TTT AAA AAT GGT GGC TCC AAC GTA GTT (PRO Ser Phe Lys Asn Gly Gly Ser Asn Val Val AAT GAC ATG TCG TCA CCG TTT GCA ATC GAC GGA (Asn Asp Met Ser Ser Pro Phe Ala Ile Asp Gly 20 25 AAC GGT CAT TCG TTA CTG TCC GAT GTT CCT GAG (Asn Gly His Ser Phe Leu Ser Asp Val Pro Glu 35 40 45 CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG (PRO Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro C PRO Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro C PTO Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro C PTO Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro C TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT AGC S Phe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser 70 G ATT GGG AAG CTG AAG GAT ATT CCG TTT ATG AGT	Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala Ser G To 10 Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: Asp Gln Asp Gln Met Val Val Val Gln Val Pro Trp: 5 10 INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2517 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (Cucumis sativas) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTTCTT CTTTTCTT CCT AGT TTT AAA AAT GGT GGC TCC AAC GTA GTT TCA APO Ser Phe Lys Asn Gly Gly Ser Asn Val Val Ser (A) CAST GTC TCA CCG TTT GCA ATC GAC GGA TCG (A ASN Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser (B) AAT GAC ATT TCG TCA CCG TTT GCA ATC GAC GAT CGA (A ASN Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser (B) AAC GGT CAT TCG TTT CTG TCC GAT GTT CCT GAG AAC (A ASN Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser (B) AAC GGT CAT TCG TTT CTG TCC GAT GTT CCT GAG AAC (A ASN Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser (B) AAC GGT CAT TCG TTT CTG TCC GAT GTT CCT GAG AAC (A ASN Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser (B) AAC GGT CAT TCG TTT CTG TCC GAT GTT CCT GAG AAC (CTT TCT CCG TAC ACT TCG TCG GAT GTC CCG GTT (CTT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT (CTT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT (CTT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT (CTT GTT GGA TTC GAC GCG TCG GAA CCT GAT AGC CGA (CTTT GTT GGA TTC GAC GCG TCG GAA CCT GAT AGC CGA (CTTT GTT GGA ATC GAC GCG TCG GAA CCT GAT AGC CGA (CTTT GTT GGA ATC GAC GCG TCG GAA CCT GAT AGC CGA (CTTT GGG AAC CTG AAG GTT ATT CGG TTT ATG AGT ATT	Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala Ser Glu P 5 10 Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: Asp Gln Asp Gln Met Val Val Gln Val Pro Trp Pro 5 10 INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2517 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (Cucumis sativas) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTCTT CTTTCTTCT CTTTCTTCT CTTCTTCTT CTTCTT	Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro A 5 10 15 Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: Asp Gln Asp Gln Met Val Val Gln Val Pro Trp Pro 5 10 INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2517 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (Cucumis sativas) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTTCTT CTTTCTTCT CACAA CCT AGT TTT AAA AAT GGT GGC TCC AAC GTA GTT TCA TTT GAT Pro Ser Phe Lys Asn Gly Gly Ser Asn Val Val Ser Phe Asp 10 AAT GAC ATG TCG TCA CCG TTT GCA ATC GAC GGA TCG GAT TTC ASN ASP Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe 20 25 AAC GGT CAT TCG TCA CCG TTT GCA ATC GAC GGA TCG GAT TTC ASN Gly His Ser Phe Leu Ser Asp Val Pro Glu Asn Ile Val 35 40 GCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CGG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CGG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC GAT ACC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC GAT ACC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC GAT ACC CCG GTT TCG GTT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC GAT ACC CCG GTT TCG GTT CTT GTT GGA AGC CTG AAG GAT ATT CCG TTT ATG AAGT ATT TTC AGG ATT GGG AAG CTG AAG CTG AAG CTT ATT TTC AAG	Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp 5 10 15 Arg His INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (v) FRAGMENT TYPE: internal (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: Asp Gln Asp Gln Met Val Val Val Gln Val Pro Trp Pro 5 10 INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2517 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (vi) ORIGINAL SOURCE: (A) ORGANISM: cucumber (Cucumis sativas) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 562407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTTCTT CTTTTCTTC CACAA ATG Met Pro Ser Phe Lys Asn Gly Gly Ser Asn Val Val Ser Phe Asp Gly AAAT GAC ATG TCG TCA CCG TTT GCA ATC GAC GAT TCG GAT TCC ACT ACT ASN ASP Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe Thr 20 25 30 AAAC GGT CAT TCG TTC CTG TCC GAT GTC CTG GAT ACT GCT ASN ASP Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe Thr 20 25 30 AAAC GGT CAT TCG TTT CTG TCC GAT GTC CTG GAT ACT GCT ASN ASP Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe Thr 20 25 30 AAAC GGT CAT TCG TTT CTG TCC GAT GTC CTG GAT TCC GCT ASN ASP Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe Thr 20 25 30 AAAC GGT CAT TCG TTT CTG TCC GAT GTC CTG GAT TCC GCT ASN Gly His Ser Phe Leu Ser Asp Val Pro Glu Asn Ile Val Ala 35 40 45 CCT TCT CCC GTAC ACT TCG ATA GAC AAG TCC GCG GTT TCG GTT CTTT GTT GGA TTC GGT TCG GTT GCT ASN Gly His Ser Phe Leu Ser Asp Val Pro Glu Asn Ile Val Gly 55 CTTT GTT GGA TCC GAC GT TCG GAA CCT GAT GTT CTG TCG GTA CGC TCG GAA CCT GAT AGC CGA CAT GTT SPHe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser Arg His Val Val

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		260	)				265	•					70					
				CAA														922
Va:	l Ala	Gly	r Glu	ı Gln	Met	Pro	Cys	Arg	j Lev	ı Leı	ı Ly	s P	he	Glr	Gl	u As	sn	
	275					280					28							•
TAG	CAAA	TTC	CGI	GAC	TAC	GTC	'AA	CCC	CAAC	GC	C AC	C G	GC	CCC	CG	A G	CC	970
Tv:	r Lvs	Phe	e Arc	a Asp	Tyr	. Val	Asr	Pro	b Lys	s Al	a Th	r G	ly	Pro	) Ar	g A	la	
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		AAC	3 GGC	TA E			TT	r ATA	A GA	r ga	A CI	'C A	AA	GGZ	A GA	G T	${f T}{f T}$	1018
				Met														
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				c ccc														1114
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				TCA														1162	
ln	Pro	Val	Leu	Ser	Pro	Gly	Leu	Gln	Met	Thr	Met	Glu	Ası	, I	.eu	Ala			
	355					360					365								
				GTT														1210	
al	Asp	Lys	Ile	Val	Leu	His	Lys	Val	Gly	Leu	Val	Pro	Pro	0	3lu	Lys	}		
70					375					380						385			
				TAC														1258	
.la	Glu	Glu	Met	Tyr	Glu	Gly	Leu	His		His	Leu	Glu	ı Ly			Gly	7		
				390					395						400		_	1206	
				AAG														1306	
le	Asp	Gly		Lys	Ile	Asp	Val		His	Leu	ьeu	GIU			Leu	Cys	5		
	~~~	m 3 M	405	GGG	202	ama	CI N TI	410	CCN	אאכי	CCA	יי ע ייי	41 ר יי		מממ	GC	<b>\</b>	1354	
				Gly														1334	
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GT,		GAA	CAT	TGT	AAC		TTC	ATG	TTC	CTT	GGC	AC	G GA	A	GCT	AT	C	1450	
				Cys															
:50				-	455	•				460						46			
CT	CTT	GGT	CGT	GTT	GGT	GAT	GAC	TTT	TGG	TGC	ACG	GA	c cc	CC	TCT	GG'	r	1498	
er	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr	As	p Pr	0	Ser	Gl	У		
				470					475						480				
				ACG														1546	
/sp	Pro	Asn	_	Thr	Phe	Trp	Leu		Gly	Cys	His	s Me			Hıs	СУ	S		
			485		maa	3 ma	000	490	mmo	3 M/C				95	TGG		T	1594	
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				Thr															
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3CC			GGT	GGC	CCG	ATC	TAT	GTI	AGI	GAT	r TC	r GT	G G	GΑ	AAC	CF	T	1690	
				Gly															
530			_		535					540	_					54	_		
				CTG														1738	
Asn	Phe	. Asr	Lev	Leu	Lys	Lys	Leu	. Val			o As	p G]	Ly S	er			eu		
				550					559						560		. ~	2506	
				TAT														1786	
Arc	, Sei	: Gli	_	Tyr	. Ala	. Lev	Pro			g As	р Су	S Te				u A	sp		
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<u>rg</u>	Glu	Thr	Arg	Arg	Asn	Gln	Cys	Phe	Ser	Gln	Tyr	Ser	Lys	Arg	Val	
10					615				•	620					625	
				AAC												1978
hr	Ser	Lys	Thr	Asn	Pro	Lys	Asp	Ile	Glu	Trp	His	Ser	Gly	Glu	Asn	
		-		630		_	_		635					640		
CT	ATC	TCT	TTA	GAA	GGC	GTT	AAA	ACC	TTT	GCG	CTT	TAC	CTC	TAT	CAA	2026
ro	Ile	Ser	Ile	Glu	Gly	Val	Lys	Thr	Phe	Ala	Leu	Tyr	Leu	Tyr	Gln	
			645					650					655			
CC	AAA	AAA	CTT	ATC	CTC	TCC	AAG	CCC	TCT	CAA	GAT	CTT	GAC	ATA	GCT	2074
la	Lys	Lys	Leu	Ile	Leu	Ser	Lys	Pro	Ser	Gln	Asp	Leu	Asp	Ile	Ala	
	_	660					665					670				
															AAA	2122
eu	Asp	Pro	Phe	Glu	Phe	Glu	Leu	Ile	Thr	Val	Ser	Pro	Val	Thr	Lys	•
	675					680					685					
TC	ATC	CAA	ACT	TCT	CTA	CAC	TTT	GCC	CCA	TTA	GGG	CTG	GTG	AAC	ATG	2170
∘eu	Ile	Gln	Thr	Ser	Leu	His	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn	Met	
90					695					700					705	
															CTA	2218
₁eu	Asn	Thr	Ser	Gly	Ala	Ile	Gln	Ser			Tyr	Asp	Asp		Leu	
				710					715					720		
															TTT	2266
er	Ser	Val			Gly	Val	Lys			Gly	Glu	Met			Phe	
			725					730					735			
;CA	TCG	AAA	AAA .	CCA	AGG	GCT	TGT	CGT	, VLI	GAI	GGG	GAC	GAT	GTI	. GGG	2314
ıla	Ser			Pro	Arg	Ala			Ile	Asp	GLY			Val	Gly	
		740					745					750		T CC		2262
TC	AAG	rat :	GAI	, CAG	GAC	CAA	ATG	GTC	GTC	GTI	' CAA	GTG	CCA	TGG	CCA	2362
?he			Asp	Gln	Asp			Val	. Val	. Val			Pro	Tr	Pro	
	755					760					765	•			n	2407
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	CAATTTTTAT TTATGTAAGC TCAATGATTG TTGTTGTTGT CGCTGTTGTT GCTATCAATG											2517				
[A]	FATTTCTCTC CAAAAGAAAA TTATGTGTAA TTTGGAGAGT AATTAAGTGA											2517				

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 784 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

 Met
 Ala
 Pro
 Ser
 Phe
 Lys
 Asn
 Gly
 Gly
 Ser
 Asn
 Val
 Val
 Ser
 Phe
 Asp

 Gly
 Leu
 Asn
 Asp
 Met
 Ser
 Ser
 Pro
 Phe
 Ala
 Ile
 Asp
 Gly
 Ser
 Asp
 Phe

 Thr
 Val
 Asn
 Gly
 His
 Ser
 Phe
 Leu
 Ser
 Asp
 Val
 Pro
 Glu
 Asn
 Ile
 Val

 Ala
 Ser
 Pro
 Ser
 Pro
 Tyr
 Thr
 Ser
 Ile
 Asp
 Lys
 Ser
 Pro
 Val
 Ser
 Val

3ly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser Arg His Val Val Ser Ile Gly Lys Leu Lys Asp Ile Arg Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Arg Asn Gly Gly Asp Leu Glu Ser Glu Thr Gln Ile Val Ile Leu Glu Lys Ser Asp Ser Gly Arg Pro Tyr Val Phe Leu Leu Pro Ile Val Glu Gly Pro Phe Arg Thr Ser Ile Gln Pro Gly Asp Asp Asp Phe Val Asp Val Cys Val Glu Ser Gly Ser Ser Lys Val Val Asp Ala Ser Phe Arg Ser Met Leu Tyr Leu His Ala Gly Asp Asp Pro Phe Ala Leu Val Lys Glu Ala Met Lys Ile Val Arg Thr His Leu Gly Thr Phe Arg Leu Leu Glu Glu Lys Thr Pro Pro Gly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr Leu Thr Val His Pro Gln Gly Val Ile Glu Gly Val Arg His Leu Val Asp Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp Asp Gly Trp Gln Ser Ile Gly His Asp Ser Asp Pro Ile Thr Lys Glu Gly Met Asn Gln Thr Val Ala Gly Glu Gln Met Pro Cys Arg Leu Leu Lys Phe Gln Glu Asn Tyr Lys Phe Arg Asp Tyr Val Asn Pro Lys Ala Thr Gly Pro Arg ...a Gly Gln Lys Gly Met Lys Ala Phe Ile Asp Glu Leu Lys Gly Glu Phe Lys Thr Val Glu His Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly Gly Leu Arg Pro Gln Val Pro Gly Leu Pro Glu Ala Arg Val Ile Gln Pro Val Leu Ser Pro Gly Leu Gln Met Thr Met Glu Asp Leu Ala Val Asp Lys Ile Val Leu His Lys Val Gly Leu Val Pro Pro Glu Lys Ala Glu Glu Met Tyr Glu Gly Leu His Ala His Leu Glu Lys Val Gly Ile Asp Gly Val Lys Ile Asp Val Ile His Leu Leu Glu Met Leu Cys Glu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala Tyr Tyr Lys Ala Met Thr Lys Ser Ile Asn Lys His Phe Lys Gly Asn Gly Val Ile

la Ser Met Glu His Cys Asn Asp Phe Met Phe Leu Gly Thr Glu Ala 455 le Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro Ser 470 475 ly Asp Pro Asn Gly Thr Phe Trp Leu Gln Gly Cys His Met Val His lys Ala Asn Asp Ser Leu Trp Met Gly Asn Phe Ile His Pro Asp Trp 510 500 505 Asp Met Phe Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser 525 520 515 ing Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Lys 535 His Asn Phe Asp Leu Leu Lys Lys Leu Val Leu Pro Asp Gly Ser Ile 555 Leu Arg Ser Glu Tyr Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu 570 Asp Pro Leu His Asn Gly Glu Thr Met Leu Lys Ile Trp Asn Leu Asn 585 580 Lys Phe Thr Gly Val Ile Gly Ala Phe Asn Cys Gln Gly Gly Gry Trp 600 Lys Arg Glu Thr Arg Arg Asn Gln Cys Phe Ser Gln Tyr Ser Lys Arg 615 620 Val Thr Ser Lys Thr Asn Pro Lys Asp Ile Glu Trp His Ser Gly Glu 635 630 Asn Pro Ile Ser Ile Glu Gly Val Lys Thr Phe Ala Leu Tyr Leu Tyr 645 650 31n Ala Lys Lys Leu Ile Leu Ser Lys Pro Ser Gln Asp Leu Asp Ile 670 665 Ala Leu Asp Pro Phe Glu Phe Glu Leu Ile Thr Val Ser Pro Val Thr 680 685 Lys Leu Ile Gln Thr Ser Leu His Phe Ala Pro Ile Gly Leu Val Asn 695 700 Met Leu Asn Thr Ser Gly Ala Ile Gln Ser Val Asp Tyr Asp Asp Asp 710 715 Leu Ser Ser Val Glu Ile Gly Val Lys Gly Cys Gly Glu Met Arg Val 725 730 Phe Ala Ser Lys Lys Pro Arg Ala Cys Arg Ile Asp Gly Glu Asp Val 740 745 Gly Phe Lys Tyr Asp Gln Asp Gln Met Val Val Gln Val Pro Trp 760 Pro Ile Asp Ser Ser Ser Gly Gly Ile Ser Val Ile Glu Tyr Leu Phe 775 780

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
TYT	TAYCTBA CHGTNCAYCC TCA	23
2)	INFORMATION FOR SEQ ID NO:7:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
түт	TAYCTBA CHGTNCAYCC CCA	23
2)	INFORMATION FOR SEQ ID NO:8:	
-,	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
TY	TAYCTBA CHGTNCAYCC ACA	23
2)	INFORMATION FOR SEQ ID NO:9:	
-	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
TY	TAYCTBA CHGTNCAYCC GCA	23
(2)	INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 26 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	•
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(ix) FEATURE:	
	(A) NAME/KEY:	
	(B) LOCATION:	
	, = , = = = = = = = = = = = = = = = = =	

(ii) MOLECULE TYPE: other nucleic acid

	(D) OTHER INFORMATION: N at 6 and 11 = inosine Other N = A, G, C, or T	
((xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
ARGO	GNGTNM GNCAYCTRGT NGAYGG	26
2)	INFORMATION FOR SEQ ID NO:11:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 26 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(ix) FEATURE:	
	(A) NAME/KEY:	
	(B) LOCATION:	
	(D) OTHER INFORMATION: N at 6 and 11 = inosine	
	Other $N = A$, G , C , or T	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
ARG	GNGTNM GNCAYCTYGT NGAYGG	26
2)	INFORMATION FOR SEQ ID NO:12:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 26 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(ix) FEATURE:	
	(A) NAME/KEY:	
	(B) LOCATION:	
	(D) OTHER INFORMATION: N at 6 and 11 = inosine	
	Other $N = A$, G , C , or T	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	26
3ARC	GGNGTNM GNCAYTTRGT NGAYGG	26
(2)	INFORMATION FOR SEQ ID NO:13:	-
(2)	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 26 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(C) STRANDEDNESS: SINGTE (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(11) MOLECULE TYPE: Other nucleic acid (A) DESCRIPTION: /desc= "Synthetic DNA"	
	(ix) FEATURE:	
	(A) NAME/KEY:	
	(B) LOCATION:	
	(D) OTHER INFORMATION: N at 3 = inosine	
	(D) OTHER THEOREMETON. IN AC 3 - INCOME.	

	Other $N = A$, G , C , or T	•
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	26
ING	GNTGYT TYGTNGGYTT YGAYGC	20
2)	INFORMATION FOR SEQ ID NO:14:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 26 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(ix) FEATURE:	
	(A) NAME/KEY:	
	(B) LOCATION:	
	(D) OTHER INFORMATION: N at 3 = inosine	
	Other $N = A$, G , C , or T	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
TNC	GGNTGYT TYGTNGGRTT YGAYGC	26
2)	INFORMATION FOR SEQ ID NO:15:	
_ •	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 29 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	•
	(ix) FEATURE:	
	(A) NAME/KEY:	
	(B) LOCATION:	
	(D) OTHER INFORMATION: N at 9 and 11 = inosine	
	Other $N = A$, G , C , or T	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
rrv	GAYGCNT CNGARCCHGA YTCDCGNCA	29
III	GAIGCNI CNGARCCHOA IICDCONCA	
(2)	INFORMATION FOR SEQ ID NO:16:	
(2)	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 30 base pairs	
	(B) TYPE: nucleic acid	
	·	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc= "Synthetic DNA"	
	(ix) FEATURE:	
	(A) NAME/KEY:	
	(B) LOCATION:	
	(D) OTHER INFORMATION: N at 9 and 11 = inosine	
	Other $N = A$, G , C , or T	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: FYGAYGCNT CNGARCCHGA YTCDAGYCAY	30
2) INFORMATION FOR SEQ ID NO:17: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc= "Synthetic DNA" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:</pre>	
AYCARGAYC TRATGGTNGT	20
2) INFORMATION FOR SEQ ID NO:18: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc= "Synthetic DNA" (ix) FEATURE:	
(A) NAME/KEY:(B) LOCATION:(D) OTHER INFORMATION: N at 6 and 15 = inosineOther N = A, G, C, or T	·
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: CCRTCNACYA GRTGNCKNAC NCCYTC	26
(2) INFORMATION FOR SEQ ID NO:19: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc= "Synthetic DNA"</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: (B) LOCATION: (D) OTHER INFORMATION: N at 6 and 15 = inosine</pre>	
CCRTCNACRA GRTGNCKNAC NCCYTC	26
(2) INFORMATION FOR SEQ ID NO:20: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs	·

		(B)	TYPE: nucleic acid	
		(C)	STRANDEDNESS: single	
		(D)	TOPOLOGY: linear	
(i	i) :	MOLEC	ULE TYPE: other nucleic acid	
•		(A)	DESCRIPTION: /desc= "Synthetic DNA"	
(i	.x)	FEATU	JRE:	
		(A)	NAME/KEY:	
			LOCATION:	
		(D)	OTHER INFORMATION: N at 6 and 15 = inosine	
			Other $N = A$, G , C , or T	
			ENCE DESCRIPTION: SEQ ID NO:20:	
CRTCN	1ACY	A TRI	TGNCKNAC NCCYTC	26
2) TN	JEOP	Marte	ON FOR SEQ ID NO:21:	
			ENCE CHARACTERISTICS:	
,	(1)		LENGTH: 29 base pairs	
			TYPE: nucleic acid	
		• - •	STRANDEDNESS: single	
			TOPOLOGY: linear	
(5	ii)		CULE TYPE: other nucleic acid	
•	,		DESCRIPTION: /desc= "Synthetic DNA"	
(:	ix)	FEAT		
•	·		NAME/KEY:	
			LOCATION:	
		(D)	OTHER INFORMATION: N at 3 and 18 = inosine	
		,	Other $N = A$, G , C , or T	
			ENCE DESCRIPTION: SEQ ID NO:21:	
'GNCG	HGAI	RT CD	GGYTCNGA NGCRTCRAA	29
			ON FOR SEQ ID NO:22:	
	(i)		ENCE CHARACTERISTICS:	
			LENGTH: 30 base pairs	
			TYPE: nucleic acid	
			STRANDEDNESS: single	
,			TOPOLOGY: linear CULE TYPE: other nucleic acid	
, (11)		DESCRIPTION: /desc= "Synthetic DNA"	
,		FEAT		•
((XI		NAME/KEY:	
			LOCATION:	
			OTHER INFORMATION: N at 19 = inosine	
		(1)	Other $N = A$, G , C , or T	

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

RTGRCTHGAR TCDGGYTCNG ANGCRTCRAA